

Amendments to the Claims

This listing of claims replaces all prior versions, and listings, of claims in the application:

1. (previously presented) A nucleic acid reference library derived from pooled DNA from at least two sources, said library comprising a heterogeneous mixture of nucleic acid fragments, wherein

each said fragment (a) is a portion of a polymorphic subregion of a polymorphic consensus sequence derived from said pooled DNA or (b) is derived from a non-polymorphic subregion,

each of said polymorphic subregions is bounded by first restriction sites and comprises an internal polymorphic restriction site which is different from said first site;

said polymorphic consensus sequence is the theoretical sequence obtained by (i) aligning said pooled DNA to provide maximum homology, and (ii) projecting each of said restriction sites onto said sequence; and

said library is enriched for fragments of type (a) relative to type (b).

2. (previously presented) A nucleic acid reference library according to claim 1, wherein at least a subpopulation of said nucleic acid fragments further comprise oligonucleotide tags, and different nucleic acid fragments are linked to different oligonucleotide tags.

3. (previously presented) The nucleic acid reference library according to claim 2, wherein said fragments are contained within a replicable vector.

4. (previously presented) The nucleic acid reference library according to claim 2, wherein said oligonucleotide tags comprise oligonucleotides of the form:

$$S_1 S_2 S_3 \dots S_n$$

wherein each of S_1 through S_n are subunits consisting of an oligonucleotide having a length from 3 to 9 nucleotides and are selected from a minimally cross-hybridizing set, n is in the range of from 4 to 10, and said tag has a length in the range of from 12 to 60 nucleotides or base pairs.

5.-12. (canceled)

13. (original) A nucleic acid reference library of genomic DNA from a plurality of individuals comprising:

a heterogeneous mixture of restriction fragments of a first restriction endonuclease;

wherein said restriction fragments from the same locus contain members having one or more restriction site polymorphisms with respect to a second restriction endonuclease, the number of such members forming a proper subset of the total number of restriction fragments from said locus.

14. (original) A nucleic acid reference library of genomic DNA from a plurality of individuals comprising:

a heterogeneous mixture of restriction fragments of a first restriction endonuclease;

wherein said restriction fragments from the same locus contain at least one member having one or more restriction site polymorphisms with respect to a second restriction endonuclease and at least one member without said restriction site polymorphism.

15.-20. (canceled)